WHAT IS CLAIMED IS:

1. A method for diagnosing a cause or risk factor for hearing loss, comprising:

obtaining a sample from a patient;

amplifying genetic sequences found in said sample;

screening the amplified genetic sequences for the presence or absence of alleles of at least 5 loci associated with a risk for hearing loss to obtain a result of the screening; and

making a diagnosis based upon the result.

2. The method of Claim 1, wherein said amplifying is performed by polymerase chain reaction.

3. The method of Claim 1, wherein said amplifying involves the use of a primer sequence found in Tables 2-10.

4. The method of Claim 1, wherein said genetic sequences comprise sequences found in genes selected from the group consisting of CDH23, MYO7A, OTOF, SLC26A4, USH2A, KCNQ1, KCNE1, GJB2 and GJB6.

5. The method of Claim 4, wherein said genetic sequences comprise sequences of at least two adjacent exons.

6. The method of Claim 5, wherein said multiple adjacent exons are selected from the group consisting of CDH23 exons 2-3, CDH23 exons 4-6, CDH exons 7-9, CDH23 exons 10-11, CDH23 exons 12-13, CDH23 exons 14-16, CDH23 exons 17-21, CDH23 exons 22-27, CDH23 exons 28-31, CDH23 exons 32-36, CDH23 exons 37-43, CDH23 exons 44-46, CDH23 exons 47-53, CDH23 exons 53-68, GJB2 exons 1-2, GJB6 exons 1-4, KCNE1 exons 1-2, KCNQ1 exons 3-6, KCNQ1 exons 7-10, KCNQ1 exons 12-15, MYO7A exons 5-14, MYO7A exons 16-21, MYO7A exons 16-18, MYO7A exons 22-26, MYO7A exons 28-35, MYO7A exons 36-44, MYO7A exons 45-49, OTOF exons 4-5, OTOF exons 6-8, OTOF exons 9-11, OTOF exons 12-25, OTOF exons 16-25, OTOF exons 16-18, OTOF exons 16-20, OTOF exons 19-20, OTOF exons 21-25, OTOF exons 16-39, OTOF exons 26-39, OTOF exons 40-47, SLC26A4 exons 1-3, SLC26A4 exons 4-6, SLC26A4 exons 11-18, SLC26A4 exons 19-21, USH2A exons 1-3, USH2A exons 5-9, USH2A exons 10-11, USH2A exons 12-13, USH2A exons 15-16 and USH2A exons 17-20.

7. The method of Claim 4, wherein said genetic sequences comprise a single exon.

8. The method of Claim 7, wherein said single exon is selected from the group consisting of GJB2 exon 2, KCNE1 exon 3, KCNE1 exon 4, KCNQ1 exon 1, KCNQ1 exon 2, KCNQ1 exon 11, KCNQ1 exon 16, MYO7A exon 1, MYO7A exon 2, MYO7A exon 3, MYO7A exon 4, MYO7A exon 15, MYO7A exon 21, MYO7A exon 27, OTOF exon 1, OTOF exon 2, OTOF exon 3, USH2A exon 4, USH2A exon 14 and USH2A exon 21.

9. A method for diagnosing a cause or risk factor for hearing loss, comprising:

obtaining a sample from a patient;

screening said sample for the presence or absence of alleles of at least 5 loci associated with a risk for hearing loss to obtain a result of the screening, wherein said loci comprise sequences found in genes selected from the group consisting of CDH23, MYO7A, OTOF, SLC26A4, USH2A, KCNQ1, KCNE1, GJB2 and GJB6; and

making a diagnosis based upon the result.

10. The method of Claim 9, wherein the amount of genetic material in said sample is augmented before or during said screening.

11. The method of Claim 10, wherein said augmentation is amplification performed by polymerase chain reaction.

12. The method of Claim 10, wherein said augmentation involves the use of a primer sequence found in Tables 2-10.

13. The method of Claim 9, wherein said sequences found in genes selected from the group consisting of CDH23, MYO7A, OTOF, SLC26A4, USH2A, KCNQ1, KCNE1, GJB2 and GJB6 comprise sequences of at least two adjacent exons.

14. The method of Claim 13, wherein said multiple adjacent exons are selected from the group consisting of CDH23 exons 2-3, CDH23 exons 4-6, CDH exons 7-9, CDH23 exons 10-11, CDH23 exons 12-13, CDH23 exons 14-16, CDH23 exons 17-21, CDH23 exons 22-27, CDH23 exons 28-31, CDH23 exons 32-36, CDH23 exons 37-43, CDH23 exons 44-46, CDH23 exons 47-53, CDH23 exons 53-68, GJB2 exons 1-2, GJB6 exons 1-4, KCNE1 exons 1-2, KCNQ1 exons 3-6, KCNQ1 exons 7-10, KCNQ1 exons 12-15, MYO7A exons 5-14, MYO7A exons 16-21, MYO7A exons 16-18, MYO7A exons 22-26, MYO7A exons 28-35, MYO7A exons 36-44, MYO7A exons 45-49, OTOF exons 4-5, OTOF exons 6-8, OTOF

exons 9-11, OTOF exons 12-25, OTOF exons 16-25, OTOF exons 16-18, OTOF exons 16-20, OTOF exons 19-20, OTOF exons 21-25, OTOF exons 16-39, OTOF exons 26-39, OTOF exons 40-47, SLC26A4 exons 1-3, SLC26A4 exons 4-6, SLC26A4 exons 11-18, SLC26A4 exons 19-21, USH2A exons 1-3, USH2A exons 5-9, USH2A exons 10-11, USH2A exons 12-13, USH2A exons 15-16 and USH2A exons 17-20.

15. The method of Claim 9, wherein said sequences found in genes selected from the group consisting of CDH23, MYO7A, OTOF, SLC26A4, USH2A, KCNQ1, KCNE1, GJB2 and GJB6 comprise a single exon.

16. The method of Claim 15, wherein said single exon is selected from the group consisting of GJB2 exon 2, KCNE1 exon 3, KCNE1 exon 4, KCNQ1 exon 1, KCNQ1 exon 2, KCNQ1 exon 11, KCNQ1 exon 16, MYO7A exon 1, MYO7A exon 2, MYO7A exon 3, MYO7A exon 4, MYO7A exon 15, MYO7A exon 21, MYO7A exon 27, OTOF exon 1, OTOF exon 2, OTOF exon 3, USH2A exon 4, USH2A exon 14 and USH2A exon 21.

17. A diagnostic hearing loss microarray comprising at least 5 sequences that are indicative of presence or absence of an allele associated with a risk for hearing loss, wherein said sequences are selected from the group consisting of genetic sequences from CDH23, MYO7A, OTOF, SLC26A4, USH2A, KCNQ1, KCNE1, GJB2 and GJB6.

18. The microarray of Claim 17, wherein said sequences comprise multiple adjacent exons.

19. The microarray of Claim 18, wherein said multiple adjacent exons are selected from the group comprising CDH23 exons 2-3, CDH23 exons 4-6, CDH exons 7-9, CDH23 exons 10-11, CDH23 exons 12-13, CDH23 exons 14-16, CDH23 exons 17-21, CDH23 exons 22-27, CDH23 exons 28-31, CDH23 exons 32-36, CDH23 exons 37-43, CDH23 exons 44-46, CDH23 exons 47-53, CDH23 exons 53-68, GJB2 exons 1-2, GJB6 exons 1-4, KCNE1 exons 1-2, KCNQ1 exons 3-6, KCNQ1 exons 7-10, KCNQ1 exons 12-15, MYO7A exons 5-14, MYO7A exons 16-21, MYO7A exons 16-18, MYO7A exons 22-26, MYO7A exons 28-35, MYO7A exons 36-44, MYO7A exons 45-49, OTOF exons 4-5, OTOF exons 6-8, OTOF exons 9-11, OTOF exons 12-25, OTOF exons 16-25, OTOF exons 16-18, OTOF exons 16-20, OTOF exons 19-20, OTOF exons 21-25, OTOF exons 16-39, OTOF exons 26-39, OTOF exons 40-47, SLC26A4 exons 1-3, SLC26A4 exons 4-6, SLC26A4 exons 11-18, SLC26A4

exons 19-21, USH2A exons 1-3, USH2A exons 5-9, USH2A exons 10-11, USH2A exons 12-13, USH2A exons 15-16 and USH2A exons 17-20.

20. The microarray of Claim 17, wherein said sequences comprise a single exon.

21. The microarray of Claim 20, wherein said single exon is selected from the group consisting of GJB2 exon 2, KCNE1 exon 3, KCNE1 exon 4, KCNQ1 exon 1, KCNQ1 exon 2, KCNQ1 exon 11, KCNQ1 exon 16, MYO7A exon 1, MYO7A exon 2, MYO7A exon 3, MYO7A exon 4, MYO7A exon 15, MYO7A exon 21, MYO7A exon 27, OTOF exon 1, OTOF exon 2, OTOF exon 3, USH2A exon 4, USH2A exon 14 and USH2A exon 21.

22. A kit for detecting a candidate gene responsible for hearing loss comprising:

a microarray of Claim 17; and

buffers and components to be used with said microarray.

23. The kit of Claim 22, wherein the microarray comprises a solid support comprising a plurality of capture nucleotide sequences bound to the solid support, wherein said capture nucleotide sequences are representative of regions of candidate genes for hearing loss, and wherein the support of the kit is adapted to be contacted with a sample from a patient comprising target nucleic acid sequences, and wherein the contacting permits hybridization under stringent conditions of a target nucleic acid sequence and a capture nucleotide sequence representative of regions of candidate genes for hearing loss.